



XX claim 1: page 44 line 51pp: Endlish.

XX  
XX The present sequence is an enzyme exhibiting endo beta 1,4-glucanase  
XX activity (see 3.2.1.4). The enzyme is useful for degradation of  
XX cellulose containing biomass and also in detergent, paper and pulp, oil  
XX drilling, oil extraction, wine and juice, food ingredients, animal feed  
XX or textile industries, in treatment of wooden pulp, for debarking,  
XX decontamination, fibre modification, bio-pulping process and for  
XX improvement of stability of paper making pulps. It is further useful in  
XX detergent compositions for house hold or industrial laundering of  
XX textiles and garments. Polynuclear dyes including the  
XX endo beta 1,4-glucanase are useful as a tool to identify other  
XX homologous endoglucanases. The enzyme has a high specificity activity on  
XX carboxy methyl cellulose and, in contrast to other endoglucanases, the  
XX enzyme is able to degrade highly crystalline celluloses. The optimal  
XX temperature of the enzyme is at 60 plus or minus 5 and is fully active between  
XX pH 5.5 and 9.5. The enzyme can be used for total biomass degradation,  
XX which normally would need both cellulolytic enzymes (which have very  
XX little activity on carboxy methyl cellulose) and endoglucanases.

XX Sequence: 646 AA:

Query Match: 100.0%, Score 2529, 108.22, Length 646;  
Best Local Similarity: 100.0%, Ident. No. 9, 26-45;  
Matches: 400, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

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03 61 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 120  
04 86 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 145  
05 121 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 180  
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07 161 KSLAANAGVYALOKSLLLEFPAKSRKIPNSRIEMHRSGLDEKQWILGKRWYDA 240  
08 206 KSLAANAGVYALOKSLLLEFPAKSRKIPNSRIEMHRSGLDEKQWILGKRWYDA 265  
09 241 ALASVSNVYALALOKSLLLEFPAKSRKIPNSRIEMHRSGLDEKQWILGKRWYDA 300  
10 266 ALASVSNVYALALOKSLLLEFPAKSRKIPNSRIEMHRSGLDEKQWILGKRWYDA 325  
11 301 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 360  
12 326 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 385  
13 361 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 420  
14 386 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 445  
15 421 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 460  
16 446 GRIHVKPOLIMVYSAALISMSVEYKAVKESQDAALINFWATVEEFAHFAVYHMG 485

RESULT 2  
AAK47189 standard: Proteolite 666 AA.

XX AAK47189

XX 29-JUL-1994 (first entry)

XX Cellulase ABC3.

XX Cellulase, detergent 7 food: pharmaceutical water treatment;  
XX paper making; detergent 11 detergent 100, expression: water.

XX  
XX Acetolactase.

XX JN05444884 A.

XX 27-08-1994.

XX 40-MAR-1992.

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 KW hybridization assay: protein mapping, gene expression control, promoter  
 KW termination sequence  
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42.58;  $\Sigma_{\text{total}} = 1074$ ;  $\text{Mk} = 21$ ;  $\text{Lactation} = 6, 21$ ;

Matches 247; Conservative 64; Minimal class 91; Models 200; Index 449.

$$[A, S^2A, \dots, V^2A, \dots] \quad [V, \dots, V, \dots]$$
[illegible]

7. W. A. K. S. I. T. H. A. K. S. H. I. T. I. N. S. P. A. T.

*Journal of Interpersonal Violence* 26(1) 97-118  
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# THE UNIVERSITY OF CHICAGO

134 vswrnsjldqkqtetvblvlyvdqfblvrvnltvsvvsvlv

# Mathematics in Art and Architecture

[illegible]

# STATEMENT OF JAMES M. WILSON before the SUBCOMMITTEE ON ANTITRUST AND MONOPOLY

*(The following text is extremely faint and largely illegible due to extreme blurring and low contrast. It appears to be a list or index of items, possibly related to the "Bibliography" section mentioned in the header.)*

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[illegible][illegible]

Query Matchability	42.9%	Score (best)	16.21	Length	623
Host Local Similarity	44.9%	Prod. No.	1,060,112		
Matches	2,922	Conservative	6,642	Mismatches	9,221
				Indels	200
				Gaps	21





[illegible]

PR	1.4 · 10 <sup>21</sup> · 19.99;	9.905 · 01.599.45;
PR	1.8 · 10 <sup>21</sup> · 19.99;	9.905 · 01.599.84;
PR	2.1 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.41;
PR	2.1 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.77;
PR	2.1 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.68;
PR	2.1 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.77;
PR	2.1 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.14;
PR	2.1 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.15;
PR	2.2 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.80;
PR	2.2 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.81;
PR	2.2 · 10 <sup>21</sup> · 19.99;	9.905 · 01.600.84;
PR	2.5 · 10 <sup>21</sup> · 19.99;	9.905 · 01.614.04;
PR	2.5 · 10 <sup>21</sup> · 19.99;	9.905 · 01.614.05;
PR	2.5 · 10 <sup>21</sup> · 19.99;	9.905 · 01.614.05;
PR	2.6 · 10 <sup>21</sup> · 19.99;	9.905 · 01.614.59;
PR	2.6 · 10 <sup>21</sup> · 19.99;	9.905 · 01.614.60;
PR	2.6 · 10 <sup>21</sup> · 19.99;	9.905 · 01.614.61;
PR	2.6 · 10 <sup>21</sup> · 19.99;	9.905 · 01.614.61;
PR	2.8 · 10 <sup>21</sup> · 19.99;	9.905 · 01.619.92;
PR	2.8 · 10 <sup>21</sup> · 19.99;	9.905 · 01.619.92;
PR	2.9 · 10 <sup>21</sup> · 19.99;	9.905 · 01.621.42;

## Query Match

40-68; 21144-1988; 11871; 18-1111-1-42.

Test Local Similarity	35.4%	[Prod. No., 4, 6, 11]
Matches 214	Constructed 75	Matches 224
	Mismatches 90	Matches 224
		Mismatches 224

Math 116's 2.11

# THE HISTORY OF THE UNITED STATES

[illegible]

15 a l l c l s t s l r e m a l l v s s s s s y a l r v t i l s t l l l l r t o q s y p d t s s l l n t b l l l r b l l l 74

**6** - **Intermittent Explosive Disorder** (ICD-9-CM code 300.13) is characterized by recurrent episodes of disproportionate anger or aggression without obvious provocation.

[illegible]
$$(6) \quad \mathbb{P}(\text{HMC}(\text{Oval}) \vdash \text{Box}(\text{Virt}(\text{HMC}(\text{Oval})))) \leq \text{HMC}(\text{Oval}) \vdash \text{Box}(\text{Virt}(\text{HMC}(\text{Oval}))) \quad \text{Th. 117}$$

145 format that is subject to quality control and that is reported by 106

$$1 \leq i \leq \dim V_0 \quad \text{and} \quad 1 \leq j \leq \dim V_0$$

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187 v	epidemic	from west bank	in pds; and malaria 2-64
b	kothstg	-----	

162. S. I. KUTKOVA, *ANAL. SYNTHESE*, 1965, 241

245 *Journal of Probability and Statistics*, 2009

222 THOMAS V. L. CHENG AND KALANVOY BHATTACHARYA  
14. P. B. F. FOWLER, *Proc. Camb. Phil. Soc.*, **70**, 1971.

[illegible]

273 **ADAMSKI, H.** "KINETICS OF POLYMERIZATION OF VINYL MONOMERS IN THE PRESENCE OF A CATALYST." *J. POLYM. SCI. A-1* 4:103-110 (1966)

[illegible]

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558 MICHINORI SEVEN, YOUNG KIM, KIM H. FA. . . . . 117

[illegible]

49. <http://www.irs.gov/efile>

YOUNG, E. L. 1991. *Journal of Great Lakes Research* 17: 1-10.

4971 p.m. = 104497444p - 610411160t Solvay's formula for the distribution of the number of

$$\gamma_{4,2}^{\text{HVL}}(4,5) =$$

Research completed: March 6, 2002, 07:56:42

- Wed Mar 6 06:50:52 2002

us-09-576-778-10\_copy\_26\_485.mar5.rag

Page 19

Job Time: 194 sec

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RESULTS

US OR 444-702 Z  
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PRIORITY MSG 556374Z

CENTRAL INFORMATION:

APPLICANT: BROWN, Alan H.  
APPLICANT: FISCHE, Robert L.  
APPLICANT: Tashbrook, Corralto  
APPLICANT: Stinson, Gary  
TITLE OF INVENTION: Isdo 1.4 beta showase genes and their  
USE OF INVENTION: use to fruits

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend  
SHERIDAN, The Heritage Plaza, 2700 E. 27th Ave., Suite  
City: San Francisco  
STATE: California  
COUNTRY: USA

ZITE: 44105, 1492

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPILED: IBM PC compatible  
OPERATING SYSTEM: MS DOS/MS DOS  
SOFTWARE: Patcut to belgose #1.0, Version #1.40

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 55738/44-702  
FILING DATE: 04 MAY-1995

CLASSIFICATION: A.C.

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/271,884  
FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 01-07-947,436  
FILING DATE: 18-APR-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,417  
FILING DATE: 20-APR-1990

ALTERNATIVE NAME: NUCLEOTIDE  
NAME: BUSTARD, Kevin L.  
INSTITUTION NUMBER: 44-724  
REFERENCE/SEQUENCE NUMBER: 02507E 504 607ES  
TELEPHONE: (415) 544-9600  
TELEFAX: (415) 544-9043  
INTERESTING FOR SEQ ID NO: 23

SEQUENCE CHARACTERISTICS:  
LENGTH: 501 amino acids  
TYPE: amino acid

FUNCTION: fibrotic

MULTIPLE TYPE: protein

US OR 444-702 Z

Priority Match	48.68;	Score	10.24; 27	10.17	Length	5011	
Best Local Similarity	49.59;	prod. No.	4.16	1.71			
Matches	217;	Observations	105;	Indels	158;	Gaps	592

[illegible]

RESULT 5  
 US-08-271-883-2      APPLICATION 05/09/271883  
 PATENT NO. 5085545  
 GENERAL INFORMATION:  
 APPLICANT: BENNETT, ALAN H.  
 APPLICANT: FISCHER, ROBERT L.  
 APPLICANT: ZACHAROW, EDWARD  
 APPLICANT: STEVANNONI, JAMES  
 TITLE OF INVENTION: SYSTEM AND METHOD OF INVENTORIAL USES  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Townsend and Townsend Klepper and Firth  
 STREET: Steuart Street Tower, One Market Plaza  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: US  
 ZIP: 94105-1493  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.24  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 05/09/271883  
 FILING DATE: 07-01-1994  
 CLASSIFICATION: A45  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 05/07/887,416  
 FILING DATE: 10-Apr-1991







07 57 -W- YDA 60  
 08 612 -W- YDA 671  
 09 61 -W- YDA 69  
 10 672 -W- YDA 741  
 11 70 -W- YDA 78  
 12 74 -W- YDA 741  
 13 76 -W- YDA 78  
 14 79 -W- YDA 78  
 15 792 -W- YDA 850  
 16 98 -W- YDA 112  
 17 851 -W- YDA 110  
 18 118 -W- YDA 128  
 19 911 -W- YDA 970  
 20 124 -W- YDA 146  
 21 971 -W- YDA 146  
 22 147 -W- YDA 154  
 23 1089 -W- YDA 147  
 24 155 -W- YDA 169  
 25 1148 -W- YDA 1297  
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 28 176 -W- YDA 181  
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 30 182 -W- YDA 184  
 31 1328 -W- YDA 1387  
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 40 204 -W- YDA 224  
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07 224 -W- YDA 228  
 08 1686 -W- YDA 1745  
 09 229 -W- YDA 238  
 10 1746 -W- YDA 1905  
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 12 1806 -W- YDA 1965  
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 15 249 -W- YDA 264  
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 17 249 -W- YDA 273  
 18 1985 -W- YDA 2044  
 19 274 -W- YDA 291  
 20 2045 -W- YDA 2104  
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 22 2104 -W- YDA 2164  
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 33 346 -W- YDA 356  
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 35 357 -W- YDA 366  
 36 2518 -W- YDA 2577  
 37 367 -W- YDA 376  
 38 2578 -W- YDA 2637  
 39 377 -W- YDA 382  
 40 2648 -W- YDA 2697  
 41 384 -W- YDA 392  
 42 2698 -W- YDA 2757  
 43 393 -W- YDA 398

































Host Local Similarity 64.18% (Prod. No. 250-25)  
 Matches 2774; Conservative 59; Mismatches 90; Indels 83; Gaps 40

QY	1 A S	-----AEE- YPHNYATLQKSLLEFVACSSRLPENSRI NMGDSN	43
DB	8 ALLSLVTLVTLHLTKAAAY- NYGALQKALMFEPYQSGKIPPKRRNNMGDSN	65	
QY	44 HGRV VTLALGKRYALGKRVGLGKALGSAASHVYVYKVAHNSQ-----LDAAD	99	
DB	66 NMAVATLITLQVYAGHVENLPRVSLQMLAAVAFAPALERSQMGYLLDA---	122	
QY	100 NFAVATLITLQVYAGHVENLPRVSLQMLAAVAFAPALERSQMGYLLDA---	154	
DB	124 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	176	
QY	154 DAAVATLITLQVYAGHVENLPRVSLQMLAAVAFAPALERSQMGYLLDA---	204	
DB	177 LVVAAVATLITLQVYAGHVENLPRVSLQMLAAVAFAPALERSQMGYLLDA---	224	
QY	204 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	258	
DB	224 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	281	
QY	259 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	317	
DB	281 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	336	
QY	317 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	372	
DB	336 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	394	
QY	372 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	435	
DB	394 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	454	
QY	435 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	460	
DB	454 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS	460	

## RESULT 7

endo-beta-1,4-glucanase (EC 4.2.1.4) CelYOG precursor - Clostridium cellulolyticum  
 c1spec001: Clostridium cellulolyticum  
 c1data: 400-500 1993 #sequence\_revision 12-Mar-1993 #taxid\_change 21-Jul-2000  
 c1accession: J01400

Reference: J. G. Gaudin, C. J. Bolach, A. J. Hoest, P. J. Clard, T. J. Bolach, J. P. G. Gaudin, 1992

Abstract: Sequence analysis of a gene cluster encoding cellulases from Clostridium cellulolyticum. The cluster contains the genes for endo-beta-1,4-glucanase (celYOG), exo-beta-1,4-glucanase (celYOG), and endo-beta-1,4-glucanase (celYOG).

Accession: J01400  
 Accession type: DNA  
 Accession: 1725-5847

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 Accession: 1725-5847

QY 51 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

DB 82 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

QY 100 NFAVATLITLQVYAGHVENLPRVSLQMLAAVAFAPALERSQMGYLLDA---

DB 149 FIKRNPVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

QY 164 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

DB 195 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

QY 224 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

DB 251 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

QY 276 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

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QY 336 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

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QY 394 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

DB 412 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

QY 444 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

DB 470 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

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QY 459 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

DB 650 LKAVVLYLKLPDPRVNY VYKSLHLDHSHVDAVYMDKRYKYLALN PDS

RESULT 8

c1spec001: Clostridium cellulolyticum

c1data: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #taxid\_change 21-Jul-2000

c1accession: J01400

Accession: 1725-5847

Accession: 1725-5847

Accession: 1725-5847

Accession: 1725-5847

Accession: 1725-5847

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Accession: 1725-5847

Accession: 1725-5847









Wed Mar 6 06:50:57 2002

us-09-576-778-10\_copy\_26\_485.mar5.rpr

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GenCore version 4.5  
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EM protein - protein search, using sw model

[illegible]

(without diluents) 1271, 942 and 1000 cm<sup>-1</sup> (peak at 942 cm<sup>-1</sup>)

1110: 15-14 576 778 11-014V-26-485

Sequence: 1 ASAHHYPIHYALIKKSLF . . . . . VAKMQLFKKHVP1.P1PPE 460

Scoring table:

Group	0	1
KLUSIM+Z		

Source: 100059 SQS, 36664827 residues

Total number of hits satisfying chosen parameters:

Midnight in the Sex I Sect. 1: (1)

Maximum DB Seq Length: 2000000000

Post-Processing: Minimum Path (\*)

Maximum Match (iii) 3

## Listing first 45 summaries

Latitudin : 2

Prod. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

## SUMMARY

Result No.	Score	Quality	Match	Length	DB	ID
1	1467.4	73.8	6.6	1	1	GENE_BACT
2	1525.5	64.1	8.0	1	1	GENE_CHIM
3	1507.9	59.7	9.0	1	1	GENE_CHIM
4	1495.6	58.2	17.2	1	1	GENE_CALSA
5	1483.7	58.8	9.6	1	1	GENE_CHIM
6	1474.8	58.4	7.5	1	1	GENE_CHIM
7	1470.1	58.2	7.9	1	1	GENE_CHIM
8	1467.1	58.1	16.5	1	1	GENE_CHIM
9	1459.4	48.1	7.9	1	1	GENE_CHIM
10	1025.5	41.0	4.5	1	1	GENE_CHIM
11	1021.8	10.5	38.3	1	1	GENE_CHIM
12	1019.4	40.4	4.6	1	1	GENE_CHIM
13	1007.4	39.9	44.5	1	1	GENE_CHIM
14	1004.7	39.9	36.9	1	1	GENE_CHIM
15	998.5	39.5	38.9	1	1	GENE_CHIM
16	998.5	39.5	38.8	1	1	GENE_CHIM
17	996.8	39.5	28.9	1	1	GENE_CHIM
18	995.7	39.4	44.7	1	1	GENE_CHIM
19	994.8	39.4	44.4	1	1	GENE_CHIM
20	993.5	39.4	42.3	1	1	GENE_CHIM
21	992.7	39.4	41.0	1	1	GENE_CHIM
22	992.5	39.4	44.5	1	1	GENE_CHIM
23	991.8	39.4	52.7	1	1	GENE_CHIM
24	989.9	39.2	44.7	1	1	GENE_CHIM
25	988.5	39.1	45.4	1	1	GENE_CHIM
26	986.7	39.1	46.4	1	1	GENE_CHIM
27	985.7	39.0	44.8	1	1	GENE_CHIM
28	984.9	39.0	44.8	1	1	GENE_CHIM
29	984.5	39.0	44.8	1	1	GENE_CHIM
30	984.5	39.0	44.4	1	1	GENE_CHIM
31	984.1	39.0	44.4	1	1	GENE_CHIM
32	982.7	38.9	44.8	1	1	GENE_CHIM
33	981.7	38.9	44.7	1	1	GENE_CHIM

## ALL INFORMATION

[illegible]

[illegible]



[illegible]



[illegible][illegible]







[illegible][illegible]

[illegible][illegible]



16	EMBL: M4304; AA0266.1; .		
18	HSEI: F26221; AFA.		
19	IntolPro: IP001701; glyco_hydro_9.		
18	Intam: p00079; glyco_hydro_9; 1.		
18	PROSITE: P000592; GLYCOSYL_HYDROL_P1; 1.		
18	PROSITE: P000598; GLYCOSYL_HYDROL_P2; 1.		
18	GO:biological process; hydrolase; glycosidase; signal,		
KW	Enzyme: liponin.		
KW	Signal: 1	POTENTIAL	
E1	CHAIN	24	END-GLUCANASE;
E1	ACT_SITE	436	BY SIMILARITY.
E1	ACT_SITE	415	BY SIMILARITY.
E1	ACT_SITE	466	BY SIMILARITY.
E1	ACT_SITE	475	BY SIMILARITY.
E1	CONFLICT	466	DSRBIN - 2; LIPIN (IN REF. 3).
SD	SEQUENCE	496 AA; 14461 MW; 473AA159357267340 CRR04;	

2Y	487	G S WADSWORTH JOHN WALTON AND TOWNSHILL & CO.	432
14	426	JACKSON & COMPANY LIMITED LONDON	477
2Y	454	NALFINGTON & CO. LTD	

01 FAKED INTEREST: Boastful, self-laudatory statement.  
 02 SINGING: FORMS A WELL-DEVELOPED RELATIONSHIP WITH A FELLOWSHIP  
 03 ASSOCIATION FOR PROPHETIC LEADERSHIP.  
 04 SUBCULTURAL LEADERSHIP: TYPE 1 MINISTRY: PROPHET  
 05 TISSUE SUSTENTATION: Associated with the TISSUE, INFLUENCE, PERSONAL  
 06 PROPHETIC LEADERSHIP.



[illegible][illegible]



[illegible][illegible]







[illegible]

Search completed: March 5, 2002. 08:00:31  
Job time: 202 sec





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DB	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
DB	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
DB	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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[illegible]

Quarry Match	64-4#:	Score 1426-5;	39-2;	Length 887.
Best Lateral Similarity	58-8#:	Prod. No. 2,120-39;		
Martins 29#; conservative	65;	Mileage 787;	Index 75;	Caps 22.
Q9	7	SAPF--	Y-4#	NVALLKELLFEASPSH-EHNEPLNWPDSJ 42
	14			

[illegible][illegible]

K<sup>+</sup> RENIS, [ON<sup>+</sup>],  
 PA [in e<sup>+</sup>, e<sup>-</sup>, Do] H, H, ?

RP SEQUENCE FROM N.A.  
R1 STRAIN=10K7b.1;





1b: P1am: P500404; Jockey in 1; 2.  
 1b: P1am: P500759; G1yco\_hydro\_35\_1.  
 1b: P500118; H1\_HAMBY: UNKNOWN\_1.  
 2b: S200073: 7.2 AA, 62553 MW, 57116636 Da; P500045: C2004

	5.2, 9.6;	Score 135.4;	D8 2;	Length 737;
Quercy Match				
Best Local Similarity	48, 9.8;	Pred. No. 1, 30.22;		
Matchos	253;	Conservation	76;	Matchaltes
			102;	Indels
				86;
				Gaps
				37;

[illegible]

64	SITE 19
7	PDB67
8	
9	
10	
11	PDB67 PRELIMINARY; PRT: 448 AA.
12	OYB67:
13	OYB67:
14	01-JUN-2001 (ITEM67: 17, created)
15	01-JUN-2001 (ITEM67: 17, last sequence update)
16	01-JUN-2001 (ITEM67: 17, last annotation update)
17	CELLULASE.
18	Coproteomes: actinotoms.
19	Eukaryota: Metazoa: Artibeus: Artibeus: Insecta:
20	Fungi: Ascomycota: Cryptophyta: Dictyostelium: Isoprota:
21	Rhodospirillum rubrum: Rhodospirillum rubrum:
22	NCH TaxID=2654;
23	111
24	SEQUENCE FROM N.A.
25	WU C.K.?
26	"A putative cellulase gene from the Australian termite, <i>Nasutitermes</i>
27	<i>actinotomus</i> ."?
28	Submitted (JAN 2001) to the EMBL/GenBank/CCPDB databases
29	(EMBL: AF446120; DABK12439.1;
30	SEQUENCE 448 AAs: 48792 MW; GADH15076759C7A5 chr654;

Query Match	50, 48;	Score 1.270;	Lib 5;	Length 448;
Fast Local Similarity	50, 28;	Pred. No. 4, 50-22;		
Matches 240;	Conservative 64;	Mismatches 84;	Indels 100;	Gaps 42.

[illegible][illegible]



Os Nasuliler mes wälkeri



